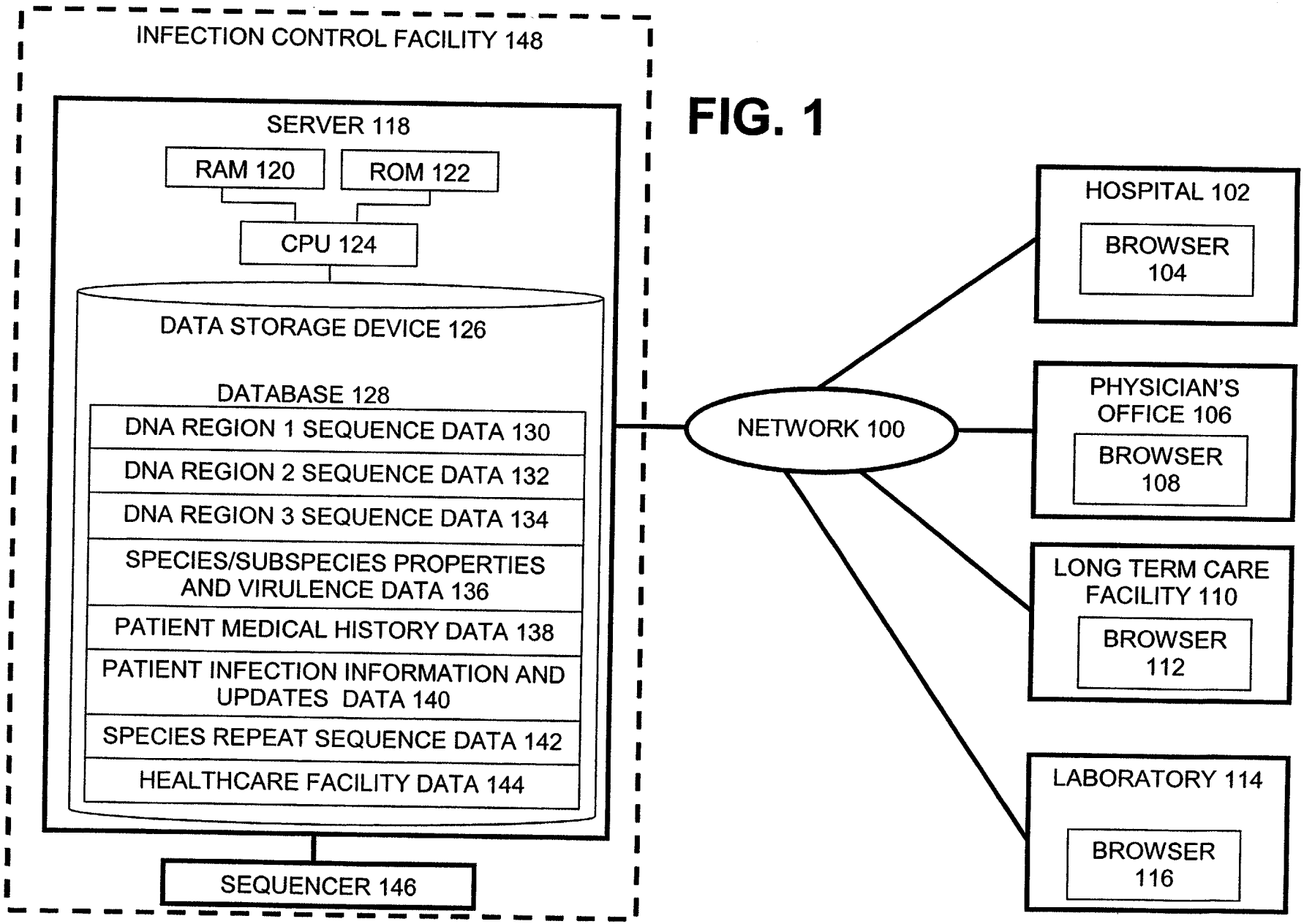
INFECTION CONTROL FACILITY 148
SERVER 118
RAM 120
ROM 122
CPU 124
DATA STORAGE DEVICE 126
DATABASE 128
DNA REGION 1 SEQUENCE DATA 130
DNA REGION 2 SEQUENCE DATA 132
DNA REGION 3 SEQUENCE DATA 134
SPECIES/SUBSPECIES PROPERTIES AND VIRULENCE DATA 136
PATIENT MEDICAL HISTORY DATA 138
PATIENT INFECTION INFORMATION AND UPDATES DATA 140
SPECIES REPEAT SEQUENCE DATA 142
HEALTHCARE FACILITY DATA 144
SEQUENCER 146
NETWORK 100
HOSPITAL 102
BROWSER 104
PHYSICIAN'S OFFICE 106
BROWSER 108
LONG TERM CARE FACILITY 110
BROWSER 112
LABORATORY 114
BROWSER 116

FIG. 1

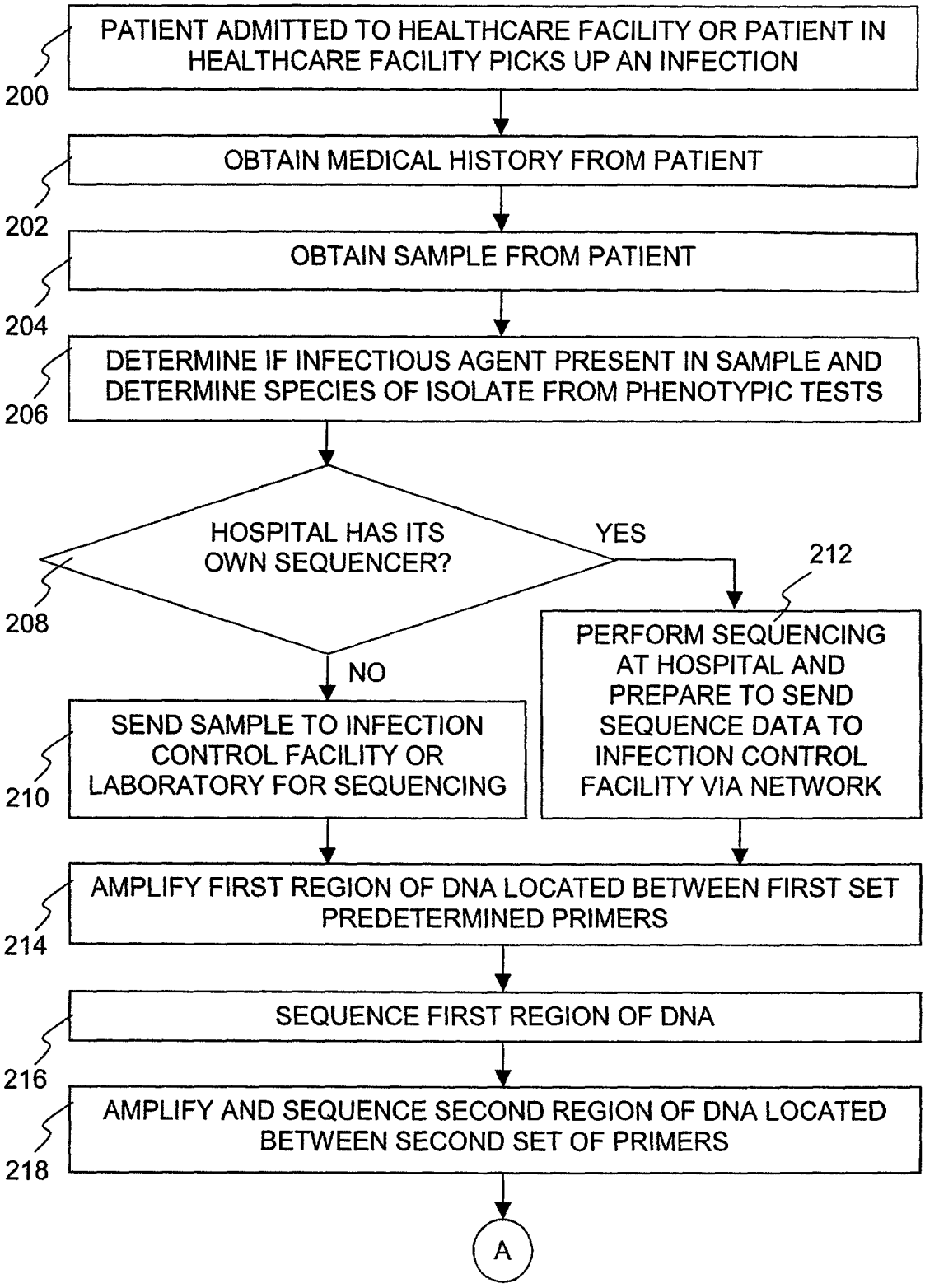
PATIENT ADMITTED TO HEALTHCARE FACILITY OR PATIENT IN HEALTHCARE FACILITY PICKS UP AN INFECTION
200
OBTAIN MEDICAL HISTORY FROM PATIENT
202
OBTAIN SAMPLE FROM PATIENT
204
DETERMINE IF INFECTIOUS AGENT PRESENT IN SAMPLE AND DETERMINE SPECIES OF ISOLATE FROM PHENOTYPIC TESTS
206
HOSPITAL HAS ITS OWN SEQUENCER?
208
YES
212
NO
PERFORM SEQUENCING AT HOSPITAL AND PREPARE TO SEND SEQUENCE DATA TO INFECTION CONTROL FACILITY VIA NETWORK
SEND SAMPLE TO INFECTION CONTROL FACILITY OR LABORATORY FOR SEQUENCING
210
AMPLIFY FIRST REGION OF DNA LOCATED BETWEEN FIRST SET PREDETERMINED PRIMERS
214
SEQUENCE FIRST REGION OF DNA
216
AMPLIFY AND SEQUENCE SECOND REGION OF DNA LOCATED BETWEEN SECOND SET OF PRIMERS
218
A

FIG. 2A

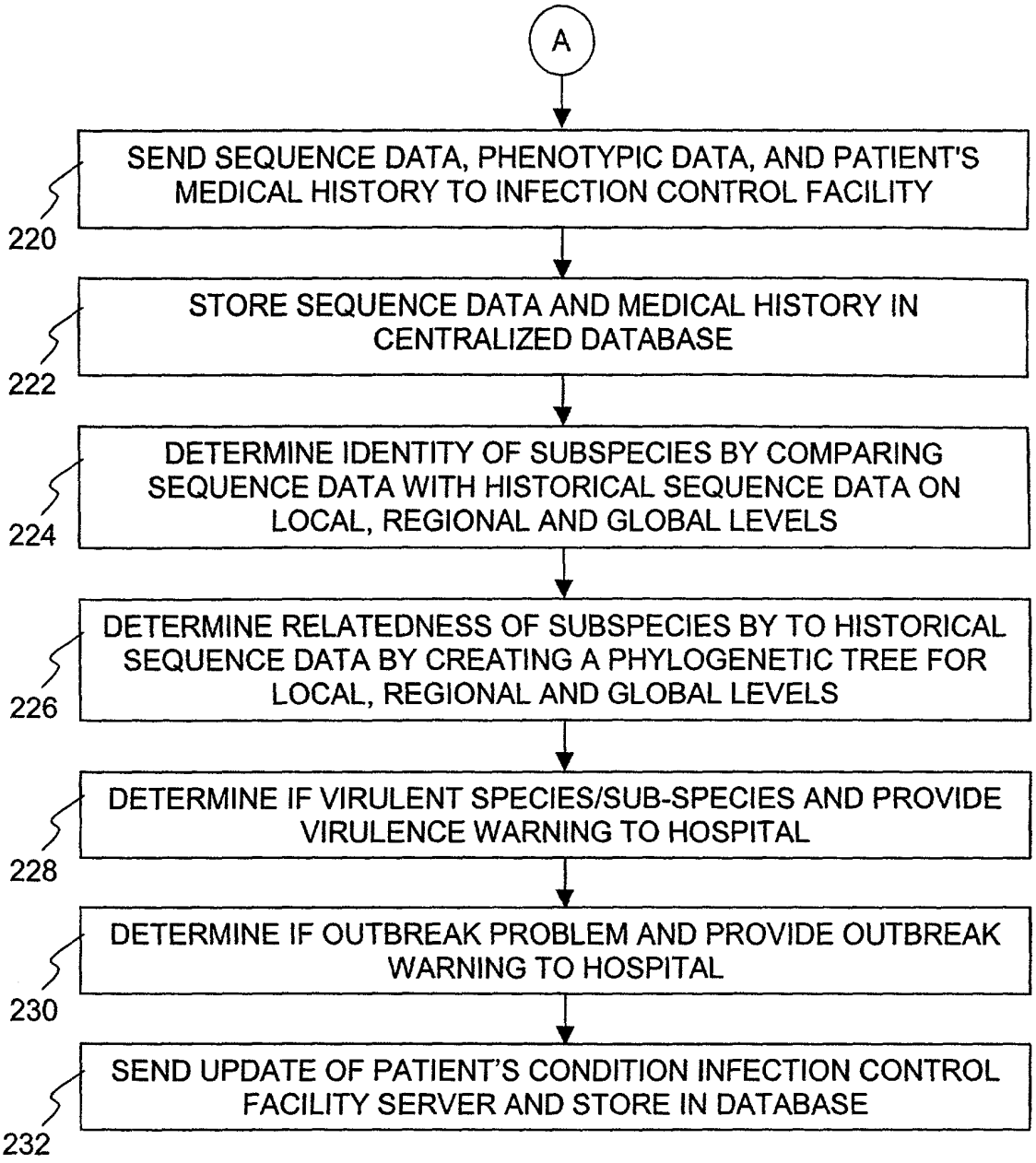
A
SEND SEQUENCE DATA, PHENOTYPIC DATA, AND PATIENT'S MEDICAL HISTORY TO INFECTION CONTROL FACILITY
220
STORE SEQUENCE DATA AND MEDICAL HISTORY IN CENTRALIZED DATABASE
222
DETERMINE IDENTITY OF SUBSPECIES BY COMPARING SEQUENCE DATA WITH HISTORICAL SEQUENCE DATA ON LOCAL, REGIONAL AND GLOBAL LEVELS
224
DETERMINE RELATEDNESS OF SUBSPECIES BY TO HISTORICAL SEQUENCE DATA BY CREATING A PHYLOGENETIC TREE FOR LOCAL, REGIONAL AND GLOBAL LEVELS
226
DETERMINE IF VIRULENT SPECIES/SUB-SPECIES AND PROVIDE VIRULENCE WARNING TO HOSPITAL
228
DETERMINE IF OUTBREAK PROBLEM AND PROVIDE OUTBREAK WARNING TO HOSPITAL
230
SEND UPDATE OF PATIENT'S CONDITION INFECTION CONTROL FACILITY SERVER AND STORE IN DATABASE
232

FIG. 2B

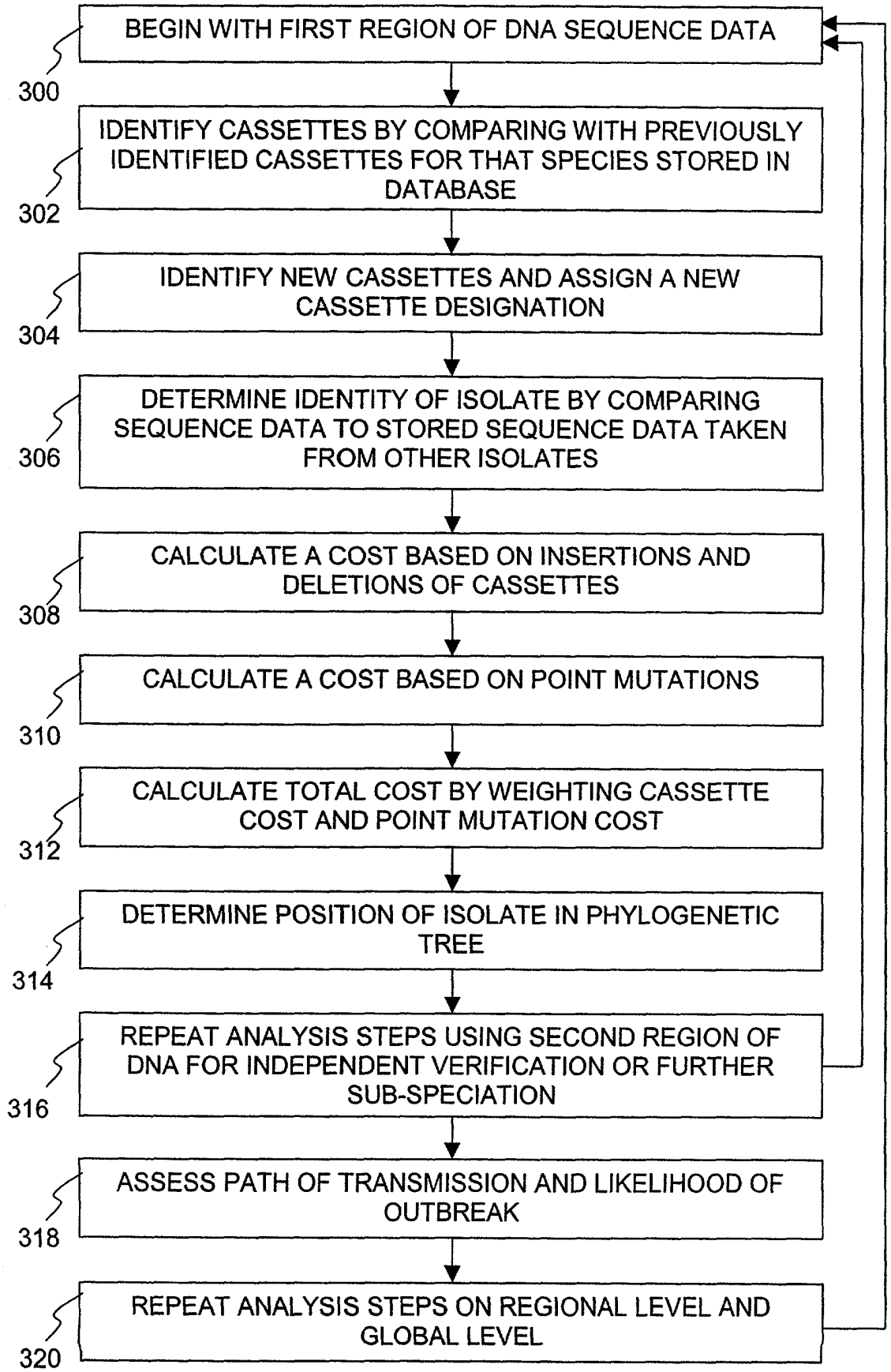
BEGIN WITH FIRST REGION OF DNA SEQUENCE DATA
300
IDENTIFY CASSETTES BY COMPARING WITH PREVIOUSLY IDENTIFIED CASSETTES FOR THAT SPECIES STORED IN DATABASE
302
IDENTIFY NEW CASSETTES AND ASSIGN A NEW CASSETTE DESIGNATION
304
DETERMINE IDENTITY OF ISOLATE BY COMPARING SEQUENCE DATA TO STORED SEQUENCE DATA TAKEN FROM OTHER ISOLATES
306
CALCULATE A COST BASED ON INSERTIONS AND DELETIONS OF CASSETTES
308
CALCULATE A COST BASED ON POINT MUTATIONS
310
CALCULATE TOTAL COST BY WEIGHTING CASSETTE COST AND POINT MUTATION COST
312
DETERMINE POSITION OF ISOLATE IN PHYLOGENETIC TREE
314
REPEAT ANALYSIS STEPS USING SECOND REGION OF DNA FOR INDEPENDENT VERIFICATION OR FURTHER SUB-SPECIATION
316
ASSESS PATH OF TRANSMISSION AND LIKELIHOOD OF OUTBREAK
318
REPEAT ANALYSIS STEPS ON REGIONAL LEVEL AND GLOBAL LEVEL
320

FIG. 3

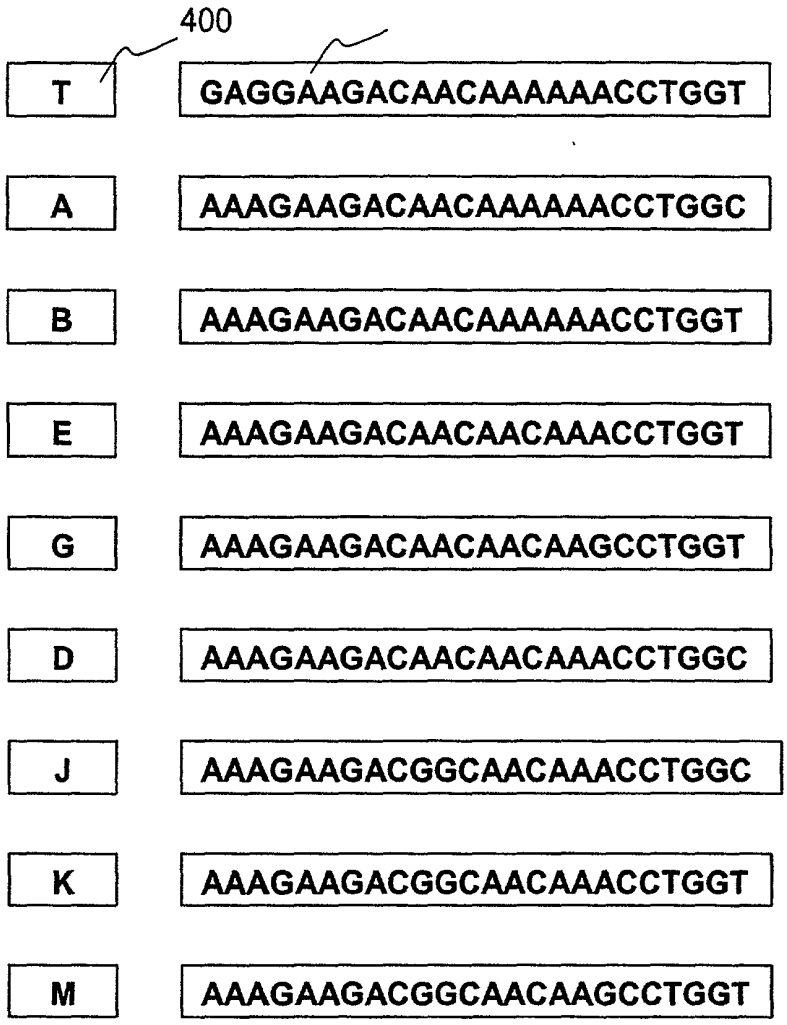

FIG. 4A

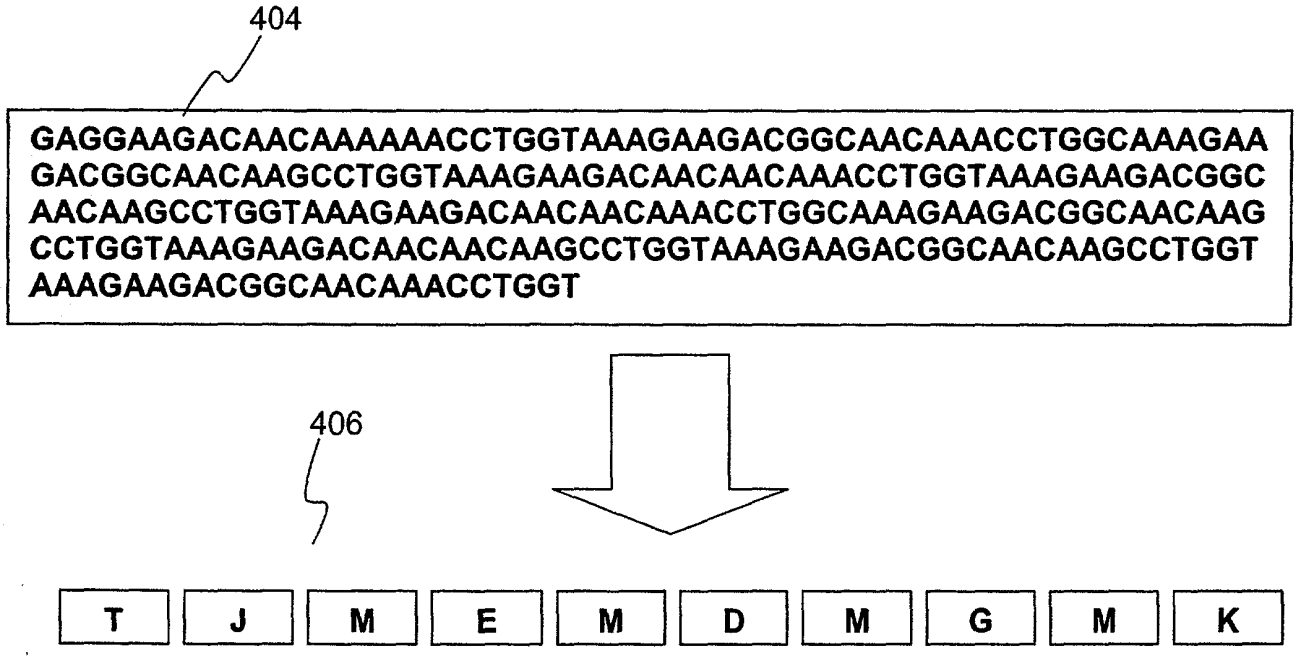

FIG. 4B

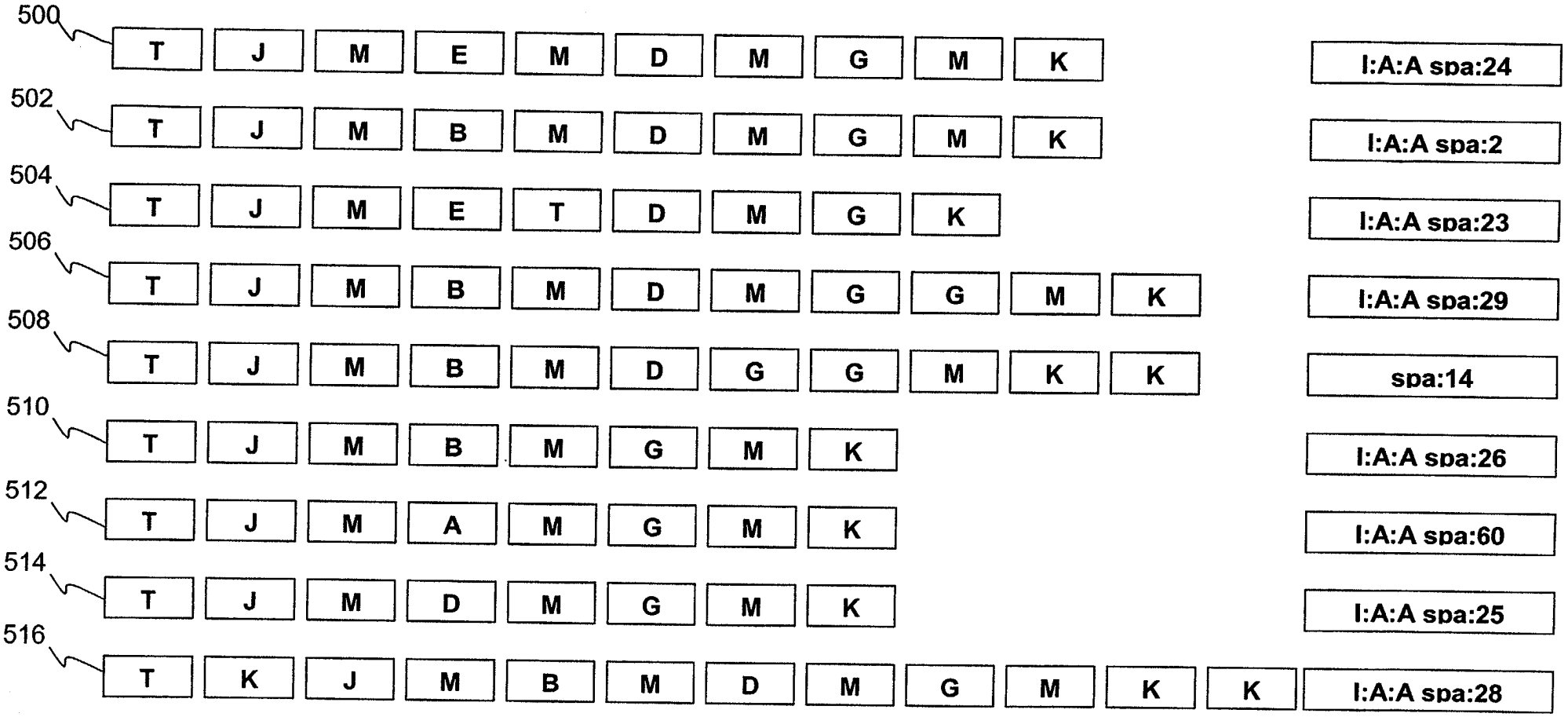
500
T J M E M D M G M K
I:A:A spa:24
502
T J M B M D M G M K
I:A:A spa:2
504
T J M E T D M G K
I:A:A spa:23
506
T J M B M D M G G M K
I:A:A spa:29
508
T J M B M D G G M K K
spa:14
510
T J M B M G M K
I:A:A spa:26
512
T J M A M G M K
I:A:A spa:60
514
T J M D M G M K
I:A:A spa:25
516
T K J M B M D M G M K K
I:A:A spa:28

FIG. 5

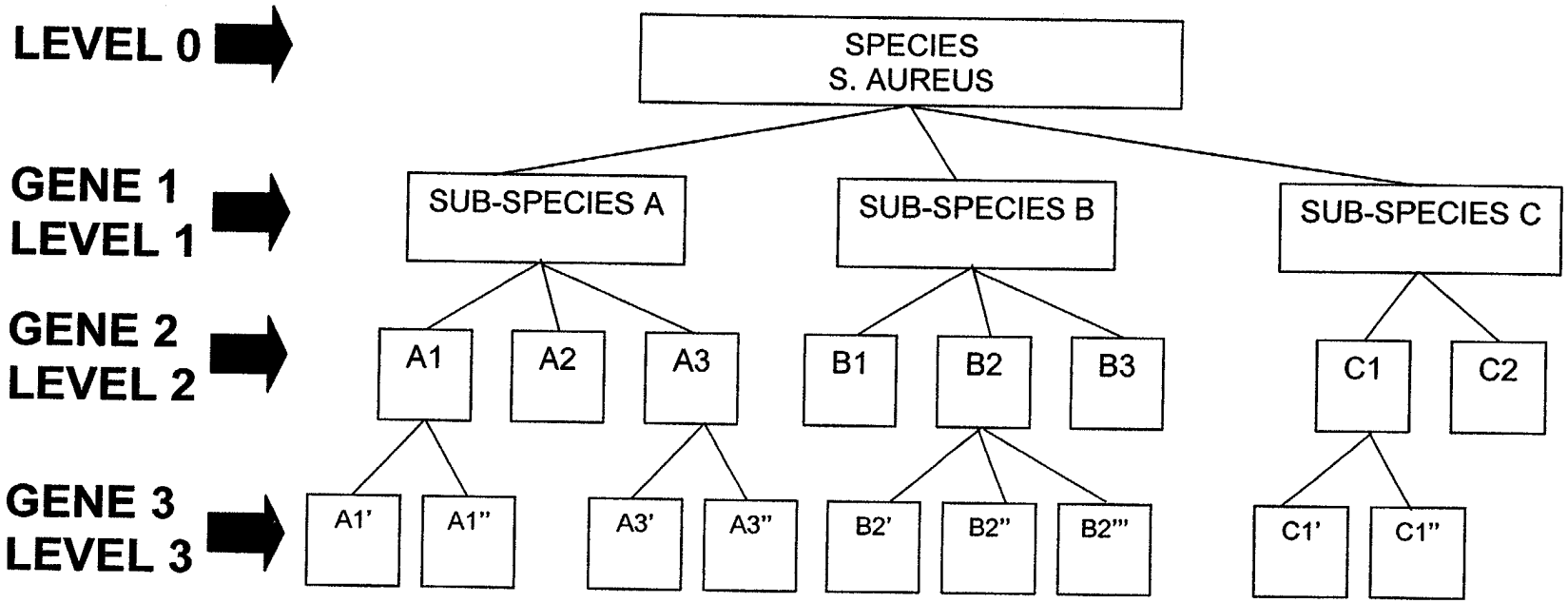
LEVEL 0
GENE 1
LEVEL 1
GENE 2
LEVEL 2
GENE 3
LEVEL 3
SPECIES
S. AUREUS
SUB-SPECIES A
SUB-SPECIES B
SUB-SPECIES C
A1
A2
A3
B1
B2
B3
C1
C2
A1'
A1"
A3'
A3"
B2'
B2"
B2'"
C1'
C1"

FIG. 6

SPECIES	S. aureus	S. aureus	
SUBSPECIES	A1'	B7"	
SEQ REGION 1	ATTCATAGAT...		
SEQ REGION 2	CGTACTATCC...		
SEQ REGION 3	ATTCGTTATA...		
REGION 1 PRIMERS			
REGION 2 PRIMERS			
REGION 3 PRIMERS			
REPEATS REGION 1	TKJMP..		
REPEATS REGION 2	ABABA		
REPEATS REGION 3	TYYT		
DATE	June 5, 2000		
PATIENT MEDICAL HISTORY	Hospitalized in New York Hospital, June 2000 for 3 weeks, heart surgery...		
PATIENT MEDICAL UPDATE INFO	Patient hospitalized 3 weeks for infection and released....	Patient died due to infection after two weeks...	
LOCATION	Mt. Sinai Hospital, Toronto, Burn Ward	New York City Hospital, ICU	
PHAGE TTYPE			

FIG. 7A

S. AUREUS			
SEQ REGION	REPEAT 1	REPEAT 2	REPEAT 3
PROTEIN A X_R	AATTCGCCTAGG.. ..	AATTCCCCTAGG..	TAGGCCGT...
REGION 2	TTAAAGGCCTGA.. .	GGTTCCAATAAT..	GGTTAACC..
REGION 3			

FIG. 7B

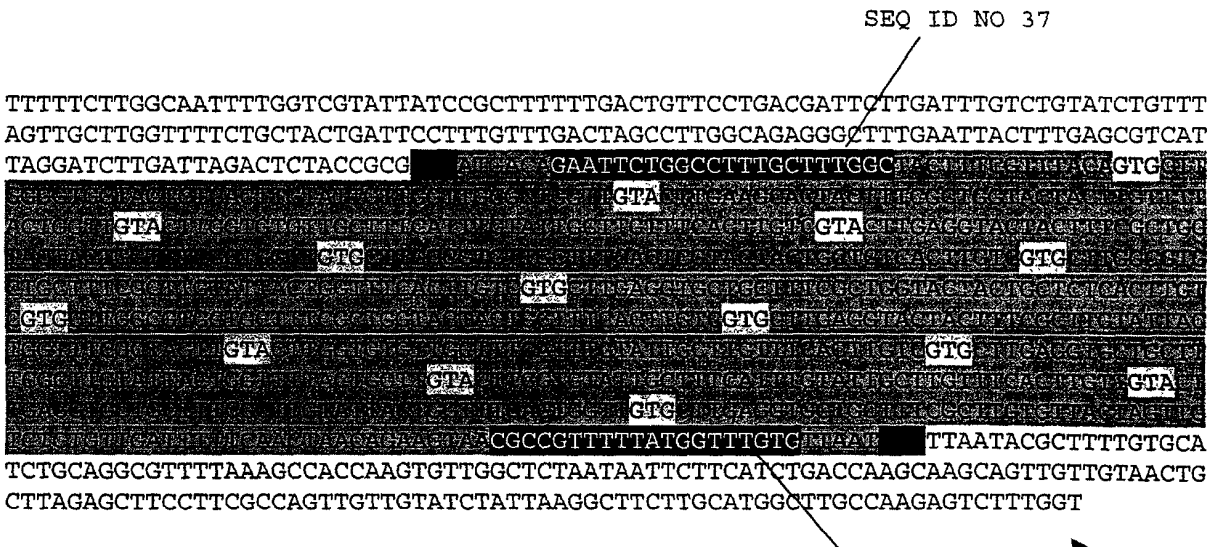

Fig. 8A

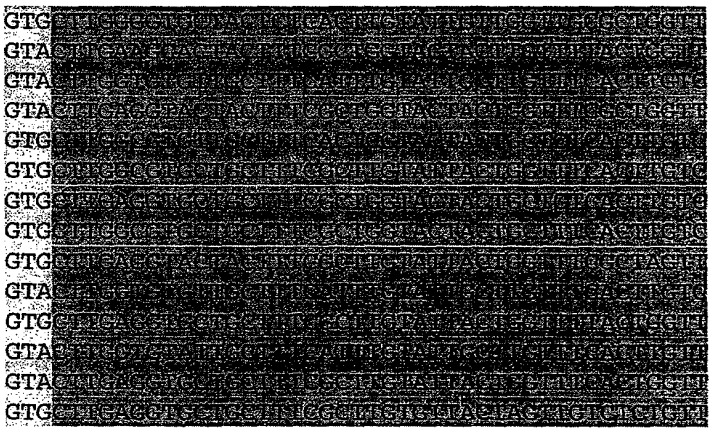

Fig. 8B

MTEFWPLLWLLSFT
VLGVLLSLVLLVALV SEQ ID NO 39
VLEALLSLVLLVLLV SEQ ID NO 40
VLGVLLSFVLLVSLV SEQ ID NO 41
VLEVLLSLVLLVSLV SEQ ID NO 42
VLGVLLSLVLLVSLV SEQ ID NO 43
VLGVLLSLVLLVSLV
VLEVLLSLVLLLSLV SEQ ID NO 44
VLGVLLSLVLLLSLV SEQ ID NO 45
VLGVLLSLVLLVSLV
VLGVLLSFVLLVSLV
VLEVLLSLVLLVLLV SEQ ID NO 46
VLGVLLSFVLLVSLV SEQ ID NO 47
VLEVLLSLVLLVSLV
VLEVLLSLVLLVVSV SEQ ID NO 48
DFSTNRSNAVFMVCVN

Fig. 8C

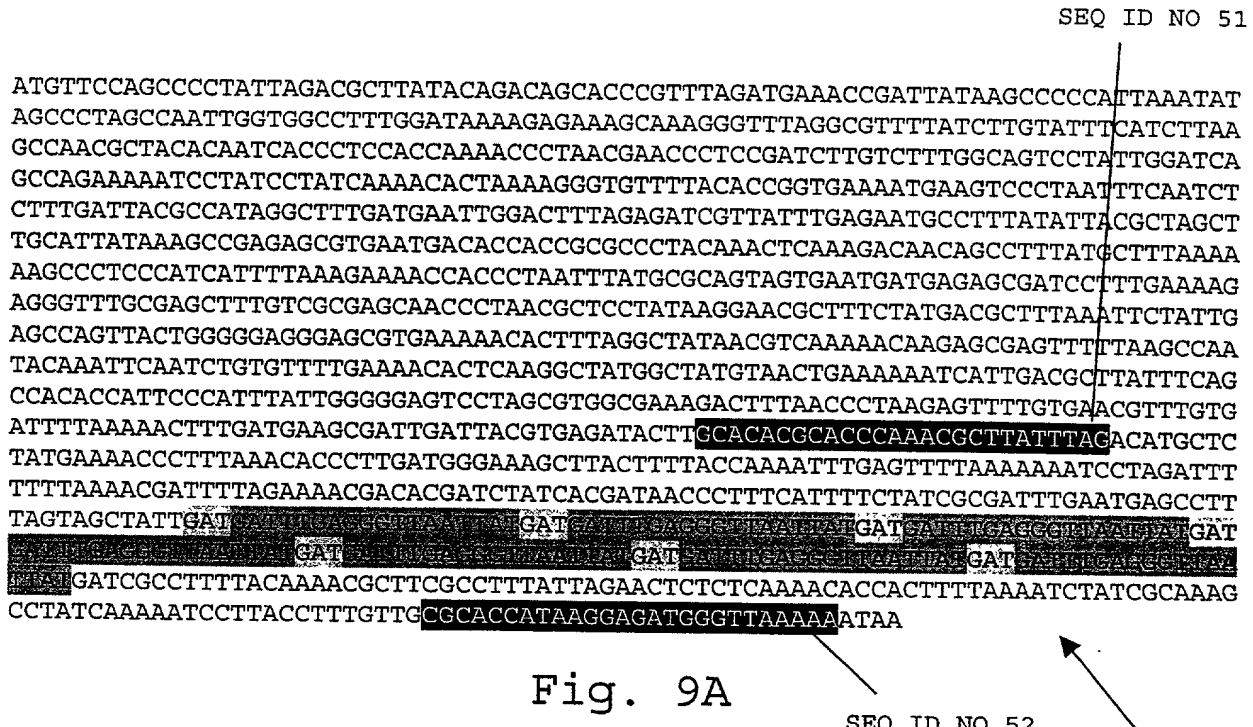

Fig. 9A

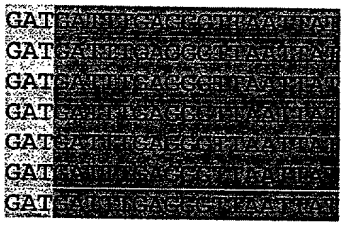

Fig. 9B

Fig. 9C

SEQ ID NO 78

PEPSPDPEPEPTPD
PEPSPDPEPEPSPD
PDP
DSDSDSDSGSDSDSGSDSDSESDSDSDSDSDSDSDSESDSDSESDSDSDSDSDSDSDSESDSDSDSDSDSD
SDSESDSDSESDSESDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSESDSDSDSDSDSDSDSDSDSDS
DSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDS
RVTPPNNEQKAPSN

Fig. 10D

SEQ ID NO 76

AATAATGAGAATGTTGTACGTTATGGTGGAAGTGCTGATGGTGATTCAGCAGTAAATCCGAAAGACCC[illegible]
GATTCGGATTCAGACAGTGACTCAGGCTCAGACAGCGACTCAGGT
TCAGATAGCGACTCAGAATCAGATAGCGATTCGGATTCAGACAGTGATTCAGATTCAGACAGCGACTCAGAATCAGA
TAGCGATTCAGAATCAGATAGCGACTCAGATTCAGATAGCGATTCAGATTCAGATAGCGATTCAGATTCAGATAGCG
ATTCGGATTCAGACAGTGATTCAGATTCAGACAGCGACTCAGAATCAGATAGCGACTCAGAATCAGATAGTGAGTCA
GATTCAGACAGTGACTCGGACTCAGACAGTGATTCAGACTCAGATAGCGATTCAGACTCAGATAGCGATTCAGATTC
AGACAGCGACTCAGATTCAGACAGCGACTCAGACTCAGATAGCGACTCAGACTCAGACAGCGACTCAGATTCAGATA
GCGATTCAGACTCAGACAGCGACTCAGACTCAGACAGCGACTCAGACTCAGATAGCGACTCAGATTCAGATAGCGAT
TCAGACTCAGACAGCGACTCAGATTCAGATAGCGATTCGGACTCAGACAGCGATTCAGATTCAGACAGCGACTCAGA
CTCGGATAGCGATTCAGATTCAGATAGCGATTCGGATTCAGACAGTGATTCAGATTCAGACAGCGACTCAGACTCGG
ATAGCGACTCAGACTCAGACAGCGATTCAGACTCAGATAGCGACTCAGACTCGGATAGCGACTCGGATTCAGATAGC
GACTCAGACTCAGATAGTGACTCCGATTCAAGAGTTACACCACCAAATAATGAACAGAAAGCACCATCAAATCCTAA
AGGTGAAGTAAACCATTCTAATAAGGTATCAAAACAACACAAAACTGATGCTTTACCA

Fig. 10A

SEQ ID NO 77

SEQ ID NO 54

AATAATGAGAATGTTGTACGTTATGGTGGTGGAAGTGCTGATGGTGATTCAGCAGTAAATCCGAAAGACCCAACTCC

GATTCGGATTCAGACAGT SEQ ID NO 55
GACTCAGGCTCAGACAGC SEQ ID NO 56
GACTCAGGTTCAGATAGC SEQ ID NO 57
GACTCAGAATCAGATAGC SEQ ID NO 58
GATTCGGATTCAGACAGT
GATTCAGATTCAGACAGC SEQ ID NO 59
GACTCAGAATCAGATAGC
GATTCAGAATCAGATAGC SEQ ID NO 60
GACTCAGATTCAGATAGC SEQ ID NO 61
GATTCAGATTCAGATAGC SEQ ID NO 62
GATTCAGATTCAGATAGC
GATTCGGATTCAGACAGT
GATTCAGATTCAGACAGC
GACTCAGAATCAGATAGC
GACTCAGAATCAGATAGT SEQ ID NO 63
GAGTCAGATTCAGACAGT SEQ ID NO 64
GACTCGGACTCAGACAGT SEQ ID NO 65
GATTCAGACTCAGATAGC SEQ ID NO 66
GATTCAGACTCAGATAGC
GATTCAGATTCAGACAGC
GACTCAGATTCAGACAGC SEQ ID NO 67
GACTCAGACTCAGATAGC SEQ ID NO 68
GACTCAGACTCAGACAGC SEQ ID NO 69
GACTCAGATTCAGATAGC
GATTCAGACTCAGACAGC SEQ ID NO 70
GACTCAGACTCAGACAGC
GACTCAGACTCAGATAGC
GACTCAGATTCAGATAGC
GATTCAGACTCAGACAGC
GACTCAGATTCAGATAGC
GATTCGGACTCAGACAGC SEQ ID NO 71
GATTCAGATTCAGACAGC
GACTCAGACTCGGATAGC SEQ ID NO 72
GATTCAGATTCAGATAGC
GATTCGGATTCAGACAGT
GATTCAGATTCAGACAGC
GACTCAGACTCGGATAGC
GACTCAGACTCAGACAGC
GATTCAGACTCAGATAGC
GACTCAGACTCGGATAGC
GACTCGGATTCAGATAGC SEQ ID NO 73
GACTCAGACTCAGATAGT SEQ ID NO 74
GACTCCGATTCAAGAGTT SEQ ID NO 75

GCACCATCAAATCCTAAAGGTGAAGTAAACCATTCTAATAAGGTATCAAAACA
ACACAAAACTGATGCTTTACCA

Fig. 10B

Repeat pattern isolate 1:
1-2-3-4-1-5-4-6-7-8-8-1-5-4-9-10-11-12-12-5-13-14-15-7-16-15-14-7-16-7-17-5-18-8-1-5-18-15-12-18-19-20-21

Fig. 10E

TCAGCAGTAAATCCGAAAGACCCAACTCCAGGGCCGCCGGTTGAC[illegible]

GATTCGGATTCAGACAGT
GACTCAGGCTCAGACAGC
GACTCAGGTTCAGATAGC
GACTCAGAATCAGATAGC
GATTCGGATTCAGACAGT
GATTCAGATTCAGACAGC
GACTCAGAATCAGATAGC
GATTCAGAATCAGATAGC
GACTCAGATTCAGATAGC
GATTCAGATTCAGATAGC
GATTCAGAATCAGATAGC
GATTCGGATTCAGACAGT
GATTCAGATTCAGACAGC
GACTCAGAATCAGATAGC
GACTCAGAATCAGATAGT
GAGTCAGATTCAGACAGT
GACTCGGACTCAGACAGT
GATTCAGACTCAGATAGC
GATTCAGACTCAGATAGC
GATTCAGACTCAGACAGC
GATTCAGATTCAGACAGC
GACTCAGAATCAGACAGC
GACTCAGACTCAGATAGC
GACTCAGACTCAGACAGC
GACTCAGATTCAGATAGC
GATTCAGACTCAGACAGC
GACTCAGACTCAGACAGC
GACTCAGACTCAGATAGC
GATTCAGACTCAGACAGC
GACTCAGATTCAGATAGC
GATTCGGACTCAGACAGC
GATTCAGATTCAGACAGC
GACTCAGACTCGGATAGC
GATTCAGATTCAGACAGC
GACTCAGACTCGGATAGC
GACTCGGATTCAGATAGT
GACTCCGATTCAAGAGTT

SEQ ID NO 79

SEQ ID NO 80

[illegible]GCACCATCAAATCCTAAAGGTCAAGTAAACCATTCTAATAAGGTATCAAAACA
ACACAAAACTGATGCTTTACCAGAAACAGGAGATAAGAGCGAAAACACAAATGCAACTTTATTTGGTGCAATG

Fig. 10C

Repeat pattern isolate 2:
1-2-3-4-1-5-4-6-7-8-6-1-5-4-9-10-11-12-12-16-5-22-14-15-7-16-15-14-16-7-17-5-18-5-18-23-21

Fig. 10F